GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:17 ; Search time 74.3927 Seconds
(without alignments)
3081.324 Million cell updates/sec

Title: US-09-937-636-4
Perfect score: 3377
Sequence: 1 MLLPLLLSSLLGGSQAMDGR.....RPEARMPKGTQADYAEVKFQ 639

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3377	100.0	639	2	AAW81023	Aaw81023 Human sia
2	3377	100.0	639	3	AAY97543	Aay97543 Human obe
3	3354	99.3	639	3	AAB25580	Aab25580 CD33-like
4	3354	99.3	639	6	ADA27052	Ada27052 Human nov
5	3354	99.3	639	8	ADE86582	Ade86582 Novel hum
6	3338	98.8	697	5	AAU87087	Aau87087 Sialic ac
7	3334	98.7	697	6	ADA27153	Ada27153 Human nov
8	3334	98.7	697	7	ADD26582	Add26582 Siglec-10
9	3334	98.7	697	8	ADI37010	Adi37010 Novel hum
10	3334	98.7	697	8	ADL82805	Adl82805 Human PRO
11	3299	97.7	622	5	AAU87075	Aau87075 Sialic ac
12	3174.5	94.0	710	7	ADD19314	Add19314 Human sec
13	2803.5	83.0	544	5	AAU87074	Aau87074 Sialic ac
14	2790.5	82.6	544	2	AAY41724	Aay41724 Human PRO
15	2790.5	82.6	544	3	AAB44280	Aab44280 Human PRO
16	2790.5	82.6	544	4	AAU29082	Aau29082 Human PRO
17	2790.5	82.6	544	6	ABU58458	Abu58458 Human PRO
18	2790.5	82.6	544	6	ABU88006	Abu88006 Novel hum
19	2790.5	82.6	544	6	ABU84321	Abu84321 Human sec
20	2790.5	82.6	544	6	ABR66195	Abr66195 Human sec
21	2790.5	82.6	544	6	ABR65585	Abr65585 Human sec
22	2790.5	82.6	544	6	ABU99525	Abu99525 Human sec
23	2790.5	82.6	544	6	ABU82764	Abu82764 Human PRO
24	2790.5	82.6	544	6	ABU89885	Abu89885 Novel hum
25	2790.5	82.6	544	6	ABR68134	Abr68134 Human sec
26	2790.5	82.6	544	6	ABU96187	Abu96187 Novel hum
27	2790.5	82.6	544	6	ABU92618	Abu92618 Human sec
28	2790.5	82.6	544	6	ABO08695	Abo08695 Human sec
29	2790.5	82.6	544	6	ABO02747	Abo02747 Human sec
30	2790.5	82.6	544	6	ABR74901	Abr74901 Human sec
31	2790.5	82.6	544	6	ABR94663	Abr94663 Human sec
32	2790.5	82.6	544	6	ABO25226	Abo25226 Novel hum
33	2790.5	82.6	544	6	ABU85636	Abu85636 Human PRO
34	2790.5	82.6	544	6	ABU98796	Abu98796 Novel hum
35	2790.5	82.6	544	6	ABU98011	Abu98011 Novel hum
36	2790.5	82.6	544	6	ABU91717	Abu91717 Novel hum
37	2790.5	82.6	544	6	ABU72232	Abu72232 Novel hum
38	2790.5	82.6	544	6	ABU89410	Abu89410 Human PRO
39	2790.5	82.6	544	6	ABU86251	Abu86251 Human sec
40	2790.5	82.6	544	6	ABU67464	Abu67464 Human sec
41	2790.5	82.6	544	6	ABU80492	Abu80492 Human PRO
42	2790.5	82.6	544	6	ABR99410	Abr99410 Human sec
43	2790.5	82.6	544	6	ABR98800	Abr98800 Human sec
44	2790.5	82.6	544	6	ABO16323	Abo16323 Human sec
45	2790.5	82.6	544	6	ABR92223	Abr92223 Human sec

ALIGNMENTS

RESULT 1
AAW81023
ID AAW81023 standard; protein; 639 AA.
XX
AC AAW81023;
XX
DT 26-APR-1999 (first entry)
XX
DE Human sialoadhesin family 4 (SAF-1) polypeptide.
XX
KW SAF-4; sialoadhesin family; human; therapy; diagnosis; cancer;
KW inflammation; autoimmune disease; allergy; asthma; inflammation;
KW cerebellar degeneration; Alzheimer's disease; Parkinson's disease;
KW multiple sclerosis, amyotrophic lateral sclerosis; head injury;
KW septic shock; sepsis; stroke; osteoporosis; osteoarthritis;
KW ischemia reperfusion injury; cardiovascular disease; kidney disease;
KW liver disease; myocardial infarction; hypotension; hypertension; AIDS;
KW myelodysplastic syndrome; aplastic anaemia; baldness; infection.
XX
OS Homo sapiens.
XX
PN WO9853840-A1.
XX
PD 03-DEC-1998.
XX
PF 27-MAY-1998; 98WO-US010791.
XX
PR 27-MAY-1997; 97US-0047572P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Kikly KK, Erickson-Miller CL;
XX
DR WPI; 1999-080779/07.
DR N-PSDB; AAV99911.
XX
PT New sialoadhesin family 4 polypetides and polynucleotides - useful to
PT treat various diseases associated with SAF-4 expression.
XX
PS Claim 1; Page 31; 48pp; English.
XX
CC This is the amino acid sequence of new human sialoadhesin family 4 (SAF-
CC 4), as deduced from the nucleotide sequence of an isolated cDNA clone
CC (see AAV99911). SAF-4 polynucleotides and polypeptides, and methods for
CC producing such polypeptides in transformed host cells using recombinant
CC techniques are disclosed. SAF-4, its agonists and antagonists, and
CC nucleic acid molecules that enhance or inhibit SAF-4 expression, may be
CC used to treat patients in need of enhancement or inhibition of SAF-4

CC expression or activity. Conditions that may benefit from such treatment
CC include cancer, inflammation, autoimmunity, allergy, asthma, rheumatoid
CC arthritis, CNS inflammation, cerebellar degeneration, Alzheimer's
CC disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral
CC sclerosis, head injury damage and other neurological disorders, septic
CC shock, sepsis, stroke, osteoporosis, osteoarthritis, ischemia reperfusion
CC injury, cardiovascular disease, kidney disease, liver disease, ischemic
CC injury, myocardial infarction, hypotension, hypertension, AIDS,
CC myelodysplastic syndromes and other haematologic abnormalities, aplastic
CC anaemia, male baldness pattern and bacterial, protozoal, fungal and viral
CC infections related to SAP-4 polypeptide activity. Methods of identifying
CC agonists, anatagonists/inhibitors are also provided, as well as
CC diagnostic assays for detecting diseases associated with inappropriate
CC SAP-4 activity or levels
XX
SQ Sequence 639 AA;

Query Match 100.0%; Score 3377; DB 2; Length 639;
Best Local Similarity 100.0%; Pred. No. 2.3e-232;
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 60

Qy         61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120

Qy        121 ERGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180

Qy        181 RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSS 240

Qy        241 HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV 300

Qy        301 LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVE 360

Qy        361 HEGEPTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 HEGEPTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWL 420

Qy        421 GEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLP 480

Qy        481 DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYI 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYI 540

Qy        541 NVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPES 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 NVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPES 600

Qy        601 QESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 639
              |||||||||||||||||||||||||||||||||||||||
Db        601 QESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 639
```

RESULT 2
AAY97543
ID AAY97543 standard; protein; 639 AA.
XX
AC AAY97543;
XX
DT 12-FEB-2001 (first entry)

XX
DE Human obesity protein binding protein-2 homologue #2.
XX
KW Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity;
KW obesity-related disorder; therapy.
XX
OS Homo sapiens.
XX
PN WO200059942-A2.
XX
PD 12-OCT-2000.
XX
PF 22-MAR-2000; 2000WO-US006682.
XX
PR 02-APR-1999; 99US-0127667P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Su EW, Wei J;
XX
DR WPI; 2000-664992/64.
DR N-PSDB; AAA37848.
XX
PT New human obesity protein binding protein-2 homologue nucleic acids,
PT polynucleotides and polypeptides useful for producing medicament for
PT treating obesity and/or obesity-related disorders.
XX
PS Claim 9; Page 89-91; 92pp; English.
XX
CC This sequence is a human obesity protein binding protein-2 homologue (hOB
CC -BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides may
CC be used for the manufacture of a medicament for the treatment of obesity
CC and/or obesity-related disorders. The hOB-BP2h nucleic acids are useful
CC as probes or amplification primers in the detection, quantification or
CC isolation of gene sequences or transcripts, for recombinant expression of
CC hOB-BP2h polypeptides, as immunogens in the preparation and screening of
CC antibodies, and in sense or antisense suppression of one or more hOB-BP2h
CC genes or nucleic acids, host cell or tissue in vivo or in vitro.
CC Antigenic epitope-bearing peptides and polypeptides are useful for
CC raising or screening antibodies that specifically binds to the hOB-BP2h
CC polypeptides
XX
SQ Sequence 639 AA;

Query Match 100.0%; Score 3377; DB 3; Length 639;
Best Local Similarity 100.0%; Pred. No. 2.3e-232;
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 60

Qy         61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120

Qy        121 ERGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180

Qy        181 RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSS 240

Qy        241 HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV 300

Qy        301 LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVE 360

Qy        361 HEGEPTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWL 420
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```
AAV99912
ID   AAV99912 standard; cDNA; 3099 BP.
XX
AC   AAV99912;
XX
DT   26-APR-1999  (first entry)
XX
DE   Human sialoadhesin family 4 (SAF-1) related EST clone.
XX
KW   SAF-4; sialoadhesin family; human; therapy; diagnosis; cancer;
KW   inflammation; autoimmune disease; allergy; asthma; inflammation;
KW   cerebellar degeneration; Alzheimer's disease; Parkinson's disease;
KW   multiple sclerosis, amyotrophic lateral sclerosis; head injury;
KW   septic shock; sepsis; stroke; osteoporosis; osteoarthritis;
KW   ischemia reperfusion injury; cardiovascular disease; kidney disease;
KW   liver disease; myocardial infarction; hypotension; hypertension; AIDS;
KW   myelodysplastic syndrome; aplastic anaemia; baldness; infection; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             51. .1249
FT                   /*tag= a
FT                   /transl_except= (pos:1176. .1177, aa:Pro)
FT                   /note= "this codon has an apparent 1 nucleotide deletion
FT                   which alters the reading frame"
XX
PN   WO9853840-A1.
XX
PD   03-DEC-1998.
XX
PF   27-MAY-1998;   98WO-US010791.
XX
PR   27-MAY-1997;   97US-0047572P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Kikly KK,  Erickson-Miller CL;
XX
DR   WPI; 1999-080779/07.
DR   P-PSDB; AAW81024.
XX
PT   New sialoadhesin family 4 polypetides and polynucleotides - useful to
PT   treat various diseases associated with SAF-4 expression.
XX
PS   Claim 13; Page 31-32; 48pp; English.
XX
CC   This is the nucleotide sequence of an expressed sequence tag (EST) clone
CC   that encodes a polypeptide (see AAW81024) which shows close homology
CC   and/or structural similarity (e.g. a conservative amino acid difference)
CC   to new human sialoadhesin family 4 (SAF-4) polypeptide (see AAW81023).
CC   SAF-4 polynucleotides and polypeptides, and methods for producing such
CC   polypeptides in transformed host cells using recombinant techniques, are
CC   disclosed. SAF-4, its agonists and antagonists, and nucleic acid
CC   molecules that enhance or inhibit SAF-4 expression, may be used to treat
CC   patients in need of enhancement or inhibition of SAF-4 expression or
CC   activity. Conditions that may benefit from such treatment include cancer,
CC   inflammation, autoimmunity, allergy, asthma, rheumatoid arthritis, CNS
CC   inflammation, cerebellar degeneration, Alzheimer's disease, Parkinson's
CC   disease, multiple sclerosis, amyotrophic lateral sclerosis, head injury
CC   damage and other neurological disorders, septic shock, sepsis, stroke,
CC   osteoporosis, osteoarthritis, ischemia reperfusion injury, cardiovascular
CC   disease, kidney disease, liver disease, ischemic injury, myocardial
CC   infarction, hypotension, hypertension, AIDS, myelodysplastic syndromes
CC   and other haematologic abnormalities, aplastic anaemia, male baldness
CC   pattern and bacterial, protozoal, fungal and viral infections related to
CC   SAF-4 polypeptide activity. Methods of identifying agonists,
CC   anatagonists/inhibitors are also provided, as well as diagnostic assays
CC   for detecting diseases associated with inappropriate SAF-4 activity or
CC   levels
XX
SQ   Sequence 3099 BP; 770 A; 907 C; 813 G; 607 T; 0 U; 2 Other;
```

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Query Match           100.0%;  Score 1917;  DB 2;  Length 3099;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 1917;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCTACTGCCACTGCTGCTGTCCTCGCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 ATGCTACTGCCACTGCTGCTGTCCTCGCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGA 110

Qy         61 TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC 170

Qy        121 TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG 230

Qy        181 TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA 290

Qy        241 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC 350

Qy        301 TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 410

Qy        361 GAGAGAGGAAGCTATGTGAGATATAATTTCATGAACGATGGGTTCTTTCTAAAAGTAACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGAGAGGAAGCTATGTGAGATATAATTTCATGAACGATGGGTTCTTTCTAAAAGTAACA 470

Qy        421 GTGCTCAGCTTCACGCCCAGACCCCAGGACCACAACACCGACCTCACCTGCCATGTGGAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GTGCTCAGCTTCACGCCCAGACCCCAGGACCACAACACCGACCTCACCTGCCATGTGGAC 530

Qy        481 TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCC 590

Qy        541 AGAGACCTTGTTATCAGCATTTCACGTGACAACACGCCAGCCCTGGAGCCCCAGCCCCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGAGACCTTGTTATCAGCATTTCACGTGACAACACGCCAGCCCTGGAGCCCCAGCCCCAG 650

Qy        601 GGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 GGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCT 710

Qy        661 GACAGCCAGCCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 GACAGCCAGCCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCC 770

Qy        721 CATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        771 CATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCA 830

Qy        781 GGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        831 GGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTC 890

Qy        841 TCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        891 TCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTC 950

Qy        901 CTGGAAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        951 CTGGAAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG 1010

Qy        961 GTCTGTGTCACACACAGCAGCCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGGTT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1011 GTCTGTGTCACACACAGCAGCCCCCCAGCCAGGCTGAGCTGGACCCAGAGGGGACAGGTT 1070

Qy       1021 CTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAG 1080
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Db       1071 CTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAG 1130

Qy       1081 CACGAAGGAGAGTTCACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGTCTCTCTC 1140

Db       1131 CACGAAGGAGAGTTCACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGTCTCTCTC 1190

Qy       1141 AGCCTCTCCGTGCACTACTCCCCGAAGCTGCTGGGCCCCTCCTGCTCCTGGGAGGCTGAG 1200

Db       1191 AGCCTCTCCGTGCACTACTCCCCGAAGCTGCTGGGCCCCTCCTGCTCCTGGGAGGCTGAG 1250

Qy       1201 GGTCTGCACTGCAGCTGCTCCTCCCAGGCCAGCCCGGCCCCCTCTCTGCGCTGGTGGCTT 1260

Db       1251 GGTCTGCACTGCAGCTGCTCCTCCCAGGCCAGCCCGGCCCCCTCTCTGCGCTGGTGGCTT 1310

Qy       1261 GGGGAGGAGCTGCTGGAGGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCAGCTCA 1320

Db       1311 GGGGAGGAGCTGCTGGAGGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCAGCTCA 1370

Qy       1321 GCCGGGCCCTGGGCCAACAGCTCCCTGAGCCTCCATGGAGGGCTCAGCTCCGGCCTCAGG 1380

Db       1371 GCCGGGCCCTGGGCCAACAGCTCCCTGAGCCTCCATGGAGGGCTCAGCTCCGGCCTCAGG 1430

Qy       1381 CTCCGCTGTGAGGCCTGGAACGTCCATGGGGCCCAGAGTGGATCCATCCTGCAGCTGCCA 1440

Db       1431 CTCCGCTGTGAGGCCTGGAACGTCCATGGGGCCCAGAGTGGATCCATCCTGCAGCTGCCA 1490

Qy       1441 GATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGAATCGGCATC 1500

Db       1491 GATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGAATCGGCATC 1550

Qy       1501 ACGGCTCTTCTTTTCCTCTGCCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGACGG 1560

Db       1551 ACGGCTCTTCTTTTCCTCTGCCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGACGG 1610

Qy       1561 ACTCAGACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCACGATCCTGGATTACATC 1620

Db       1611 ACTCAGACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCACGATCCTGGATTACATC 1670

Qy       1621 AATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGAAAGCCACACCAAAC 1680

Db       1671 AATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGAAAGCCACACCAAAC 1730

Qy       1681 AGTCCTCGGACCCCTCTTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGAAA 1740

Db       1731 AGTCCTCGGACCCCTCTTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGAAA 1790

Qy       1741 AAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAATCC 1800

Db       1791 AAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAATCC 1850

Qy       1801 CAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGG 1860

Db       1851 CAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGG 1910

Qy       1861 CCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTCCAA 1917

Db       1911 CCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTCCAA 1967
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RESULT 3
AAV99911
ID AAV99911 standard; cDNA; 3099 BP.
XX
AC AAV99911;
XX
DT 26-APR-1999 (first entry)
XX
DE Human sialoadhesin family 4 (SAF-1) cDNA.
XX
KW SAF-4; sialoadhesin family; human; therapy; diagnosis; cancer;
KW inflammation; autoimmune disease; allergy; asthma; inflammation;
KW cerebellar degeneration; Alzheimer's disease; Parkinson's disease;
KW multiple sclerosis, amyotrophic lateral sclerosis; head injury;
KW septic shock; sepsis; stroke; osteoporosis; osteoarthritis;
KW ischemia reperfusion injury; cardiovascular disease; kidney disease;
KW liver disease; myocardial infarction; hypotension; hypertension; AIDS;
KW myelodysplastic syndrome; aplastic anaemia; baldness; infection; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 51. .1970
FT /*tag= a
XX
PN WO9853840-A1.
XX
PD 03-DEC-1998.
XX
PF 27-MAY-1998; 98WO-US010791.
XX
PR 27-MAY-1997; 97US-0047572P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Kikly KK, Erickson-Miller CL;
XX
DR WPI; 1999-080779/07.
DR P-PSDB; AAW81023.
XX
PT New sialoadhesin family 4 polypetides and polynucleotides - useful to
PT treat various diseases associated with SAF-4 expression.
XX
PS Claim 2; Page 30-31; 48pp; English.
XX
CC This cDNA clone codes for new human sialoadhesin family 4 (SAF-4)
CC polypeptide (see AAW81023). It can be obtained e.g. from a cDNA library
CC derived from mRNA in cells of human primary dendritic cells, using
CC expressed sequence tag analysis. SAF-4 polynucleotides and polypeptides,
CC and methods for producing such polypeptides by recombinant techniques are
CC disclosed. SAF-4, its agonists and antagonists, and nucleic acid
CC molecules that enhance or inhibit SAF-4 expression, may be used to treat
CC patients in need of enhancement or inhibition of SAF-4 expression or
CC activity. Conditions that may benefit from such treatment include cancer,
CC inflammation, autoimmunity, allergy, asthma, rheumatoid arthritis, CNS
CC inflammation, cerebellar degeneration, Alzheimer's disease, Parkinson's
CC disease, multiple sclerosis, amyotrophic lateral sclerosis, head injury
CC damage and other neurological disorders, septic shock, sepsis, stroke,
CC osteoporosis, osteoarthritis, ischemia reperfusion injury, cardiovascular
CC disease, kidney disease, liver disease, ischemic injury, myocardial
CC infarction, hypotension, hypertension, AIDS, myelodysplastic syndromes
CC and other haematologic abnormalities, aplastic anaemia, male baldness
CC pattern and bacterial, protozoal, fungal and viral infections related to
CC SAF-4 polypeptide activity. Methods of identifying agonists,
CC anatagonists/inhibitors are also provided, as well as diagnostic assays
CC for detecting diseases associated with inappropriate SAF-4 activity or
CC levels
XX
SQ Sequence 3099 BP; 769 A; 908 C; 813 G; 607 T; 0 U; 2 Other;

Query Match 100.0%; Score 1917; DB 2; Length 3099;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1917; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGCTACTGCCACTGCTGCTGTCCTCGCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGA 60

Db         51 ATGCTACTGCCACTGCTGCTGTCCTCGCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGA 110

Qy         61 TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC 120

Db        111 TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC 170

Qy        121 TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG 180

Db        171 TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG 230
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